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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file usl.res made by msmith on rue 15 May 101 13:58:11-PDT.

Query Sequence being compared:US-09-441-723-1 (1-226)
Number of scores above cutoff:

Results of the initial comparison of US-09-441-723-1 (1-226)

Results of the initial comparison
```

	32
FARAMETERS	K-tuple Joining penalty Window size
	Unitary 1.00 0.05 1
	Similarity matrix Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group

SEARCH STATISTICS

Scores:

Standard Deviation 24.55	Total Elapsed	
Median 7		1084 6 6
18	CPU 00:00:00.00	Number of residues; Number of sequences searched; Number of scores above cutoff;
		Number of Number of Number of

The scores below are sorted by initial score. Finificance is calculated based on initial score.

100% identical sequence to the query sequence was not found.

The list of best scores is:

Frame	0	0000			04-4		.3	
Sig.	2.00	0.08 -0.41 -0.49	6.0	2.00	0 3LLEKI	220 IPPAVNA -PDFKIA	06	
Opt. Score	. 70	30 30 28	9	nce s	150 SAEQAQO	KWMGPI		
Init. Score	67		•	Significance Mismatches	40 150 160 LAAAEKAGMSAEQAOGLLEKTA	210 210 LAHLLGEKWMGPIPPAVNA 	3	
Length	76 mea 180	181 181 181 180 180			140 SILAA LAA	I		DAR
ĭ	on abov	770		70 72 72	SDITEPO	MEL MELWRT(70		LSPTPK 140
	standard deviation above mean 180 standard deviation from mean *	check: 770		Optimized Score 70 Matches 72 Conservative Substitutions	13(RVWSRNI	200 1LFGSDR 11111 1LFGSDR 60		VALGAVO 130
	dard d dard d	1397		zed Sc s vative	120 Srelww	ТВСОТНИ ВСОТНИ		LIEVES
ilon	l stan O stan			Optimized Matches Conservati	ЕМЬЕКА	190 PITVAHVI IVAHVI		GLGFLY 120
Description	: :	TOIG of:	(1-226)	67 758 11	110 AVNLEHP	180 RYGAFGLI RYGAFGLE		WLННКАL 10
	aa291397p_6 aa291397p_5	aa291397p_1 aa291397p_2 aa291397p_3 aa291397p_4	23-1	Score Identity =	90 100 110 120 130 140 150 160 SVMLEKGSLSAMRFLTAVNLEHPEMLEKASRELWMRVWSRNEDITEPQSILAAAEKAGMSAEQAQGLLEKIA [111111111111111111111111111111111111	170 180 200 210 220 191 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		RRKOTLRIKKAGHLLNPWLHHKALGLGFLYLIEVFSVALGAVCLSPTPKDAR X 100 110 140
Sequence Name	1. aa29 2. aa29	3. aa29 4. aa29 5. aa29 6. aa29	US-09-441-7 aa291397p_6	ial Jue	90 SVMLEKG:	PKVKNQI PKVKNQI	. R.	RKQTLRII X 10
Seg		, -	1. C	Initial Residue Gaps	-	r – H	~	- œ' ´`